

# multi - french

*Imperial College*

## load data

```
# from https://www.data.gouv.fr/fr/datasets/donnees-de-laboratoires-pour-le-depistage-indicateurs-sur-l
d <- read.csv(file = 'Rdata/sp-variant-7j-reg-2021-06-02-21h05.csv', sep=';')
d$reg <- as.character(d$reg)
d$cl_age90 <- as.character(d$cl_age90)
unique(d$cl_age90)

## [1] "9" "19" "29" "39" "49" "59" "69" "79" "89" "90" "0"
d$week_end <- as.Date(substr(d$semaine, 1, 10), format = '%Y-%m-%d')+6

# rename regions
f <- which(d$reg %in% c('5','7','8'))
d <- d[-f,]

# from
d_region <- read.csv(file = 'Rdata/regions-france.csv', encoding = "UTF-8")
d$region <- as.character(d_region$nom_region[match(d$reg, d_region$code_region)])
# unique(d$region)
# unique(d_region$code_region)
# sort(unique(d$reg))

# rename variants
variants0 <- c('Nb_susp_ABS', 'Nb_susp_501Y_V1', 'Nb_susp_501Y_V2_3')
# match(variants, names(d))
variants <- c('wild', 'alpha', 'beta/gamma')

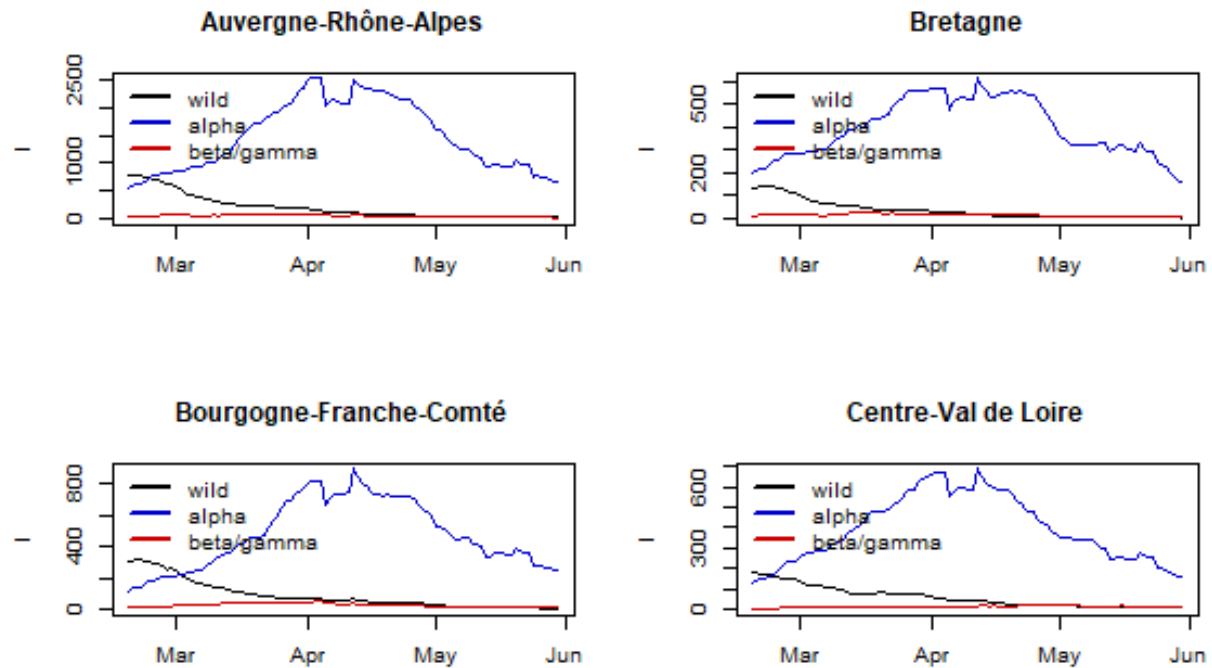
names(d) [match(variants0, names(d))] <- variants
```

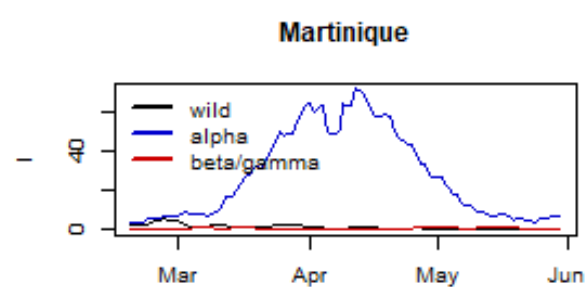
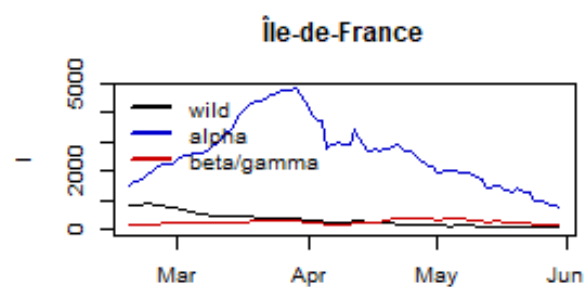
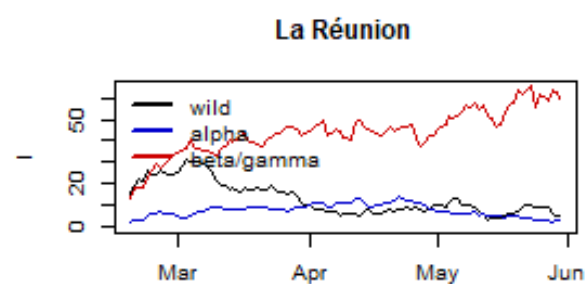
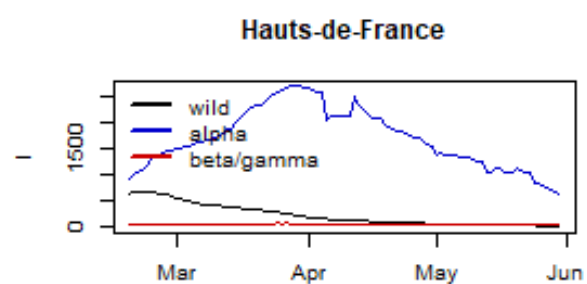
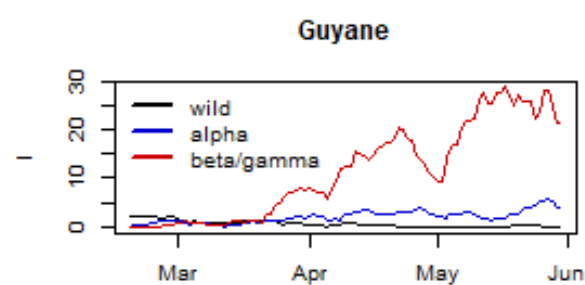
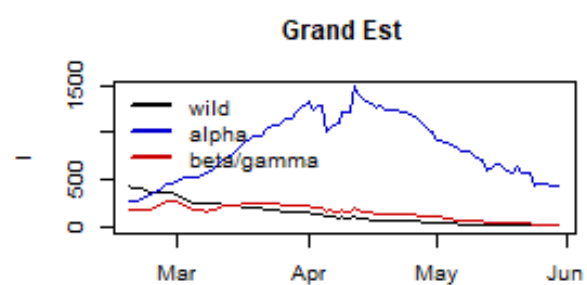
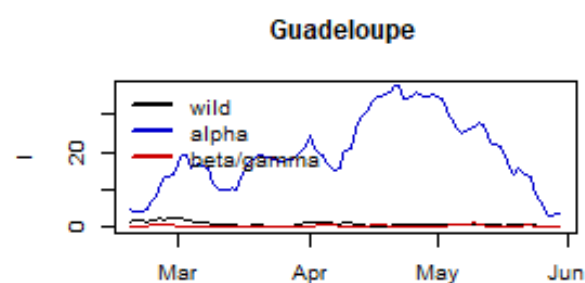
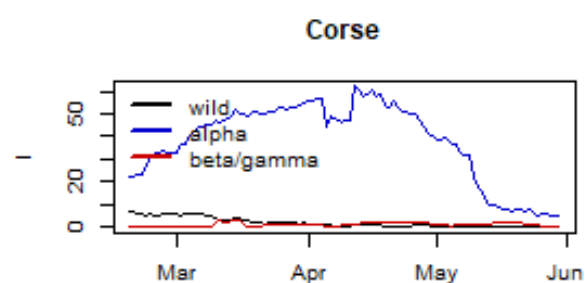
get list of matrix, 1 for each variant with 1 column for dates and ‘n’ columns for each location

```
# for incidence
regions <- sort(unique(d$region))
# for Rt
mean_prior <- c(2)
std_prior <- c(1)
#
mean_SI <- 5.4 # mean 5.4 days and standard deviation of 1.5 days (Rai, Shukla, and Dwivedi 2021).
std_SI <- 1.5
SI_assumed <- EpiEstim::discr_si(seq(0, 20), mean_SI, std_SI)
t_window <- 7
n_sample_R <- 1e1
```

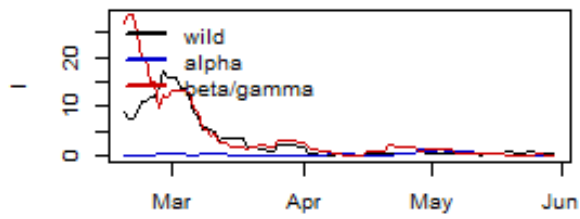
```
u_age <- unique(d$cl_age90)
```

```
initial_res <- wrapper(age_group = u_age[11] , regions = regions, plot_incidence = TRUE,  
  variants = variants, t_window = t_window,  
  SI = SI_assumed, mean_prior = mean_prior,  
  std_prior = std_prior, n_sample_R = n_sample_R, plot_Rt = TRUE)
```

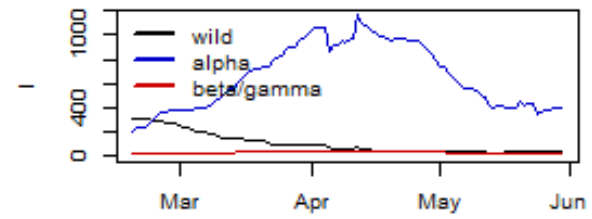




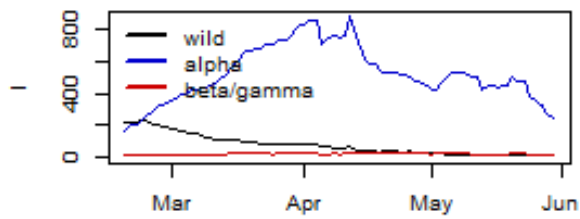
**Mayotte**



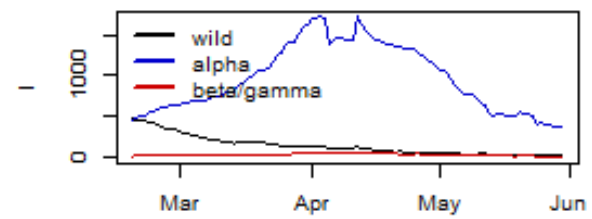
**Nouvelle-Aquitaine**



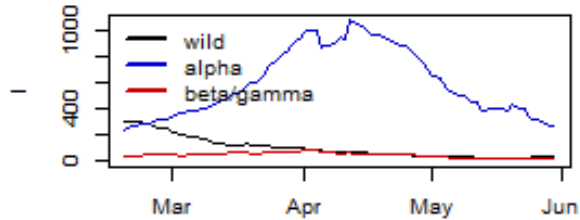
**Normandie**



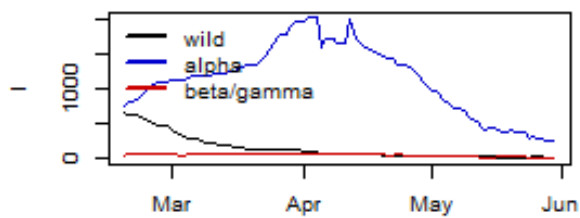
**Occitanie**

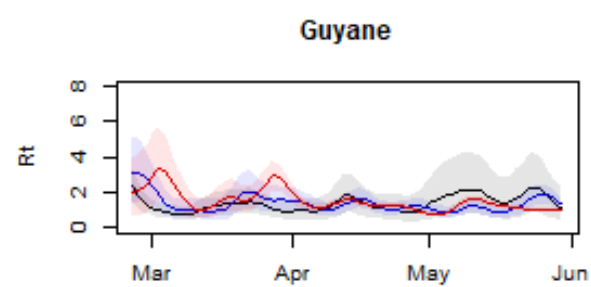
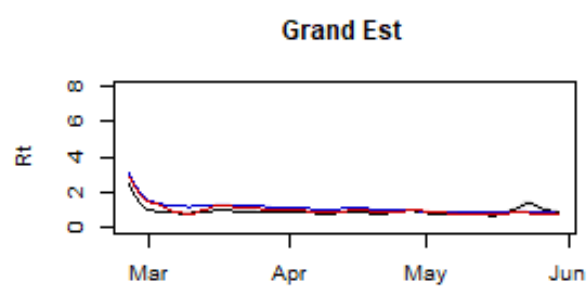
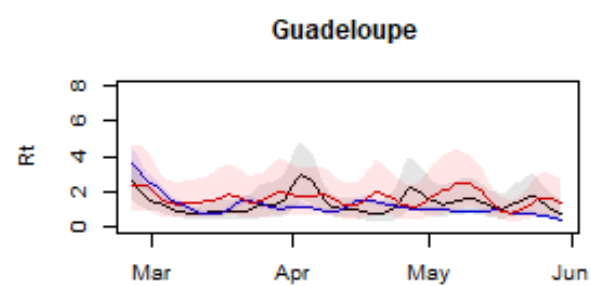
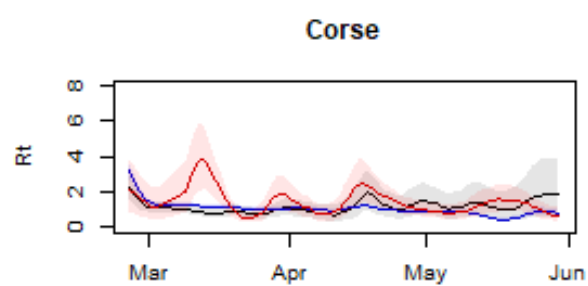
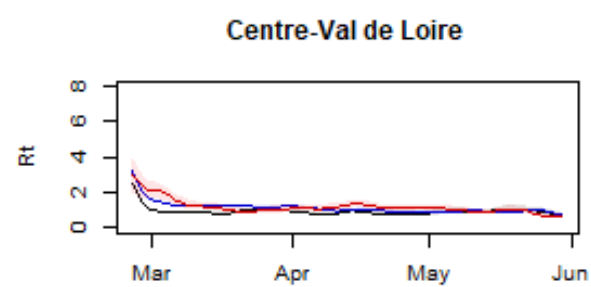
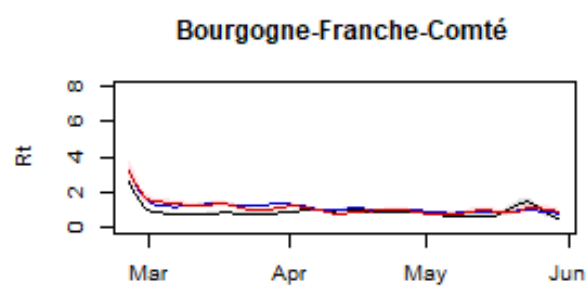
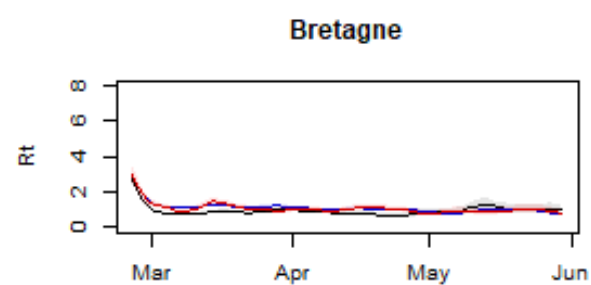
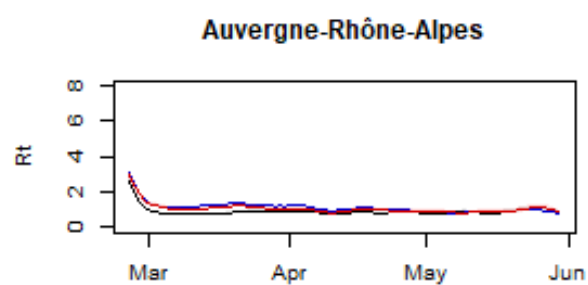


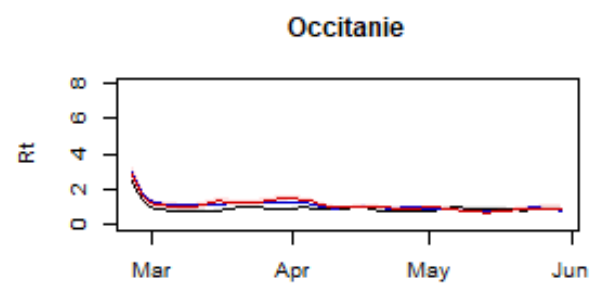
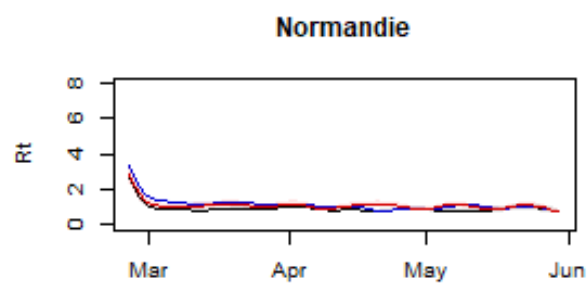
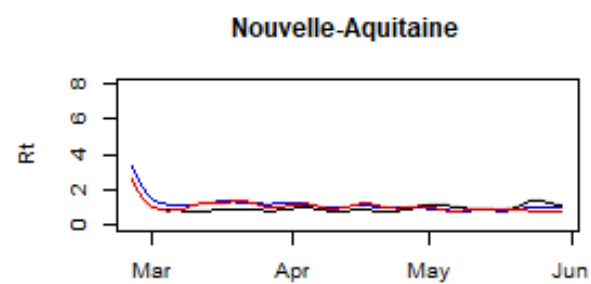
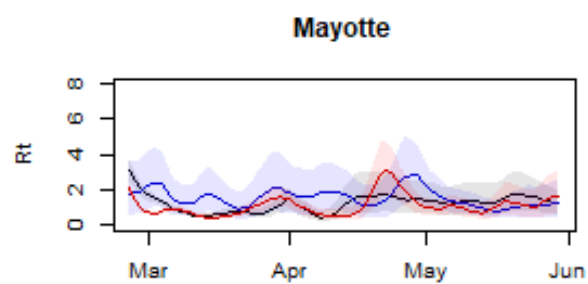
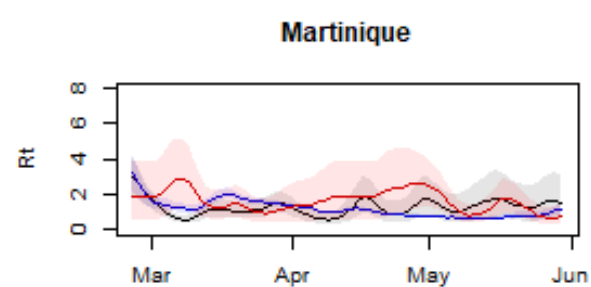
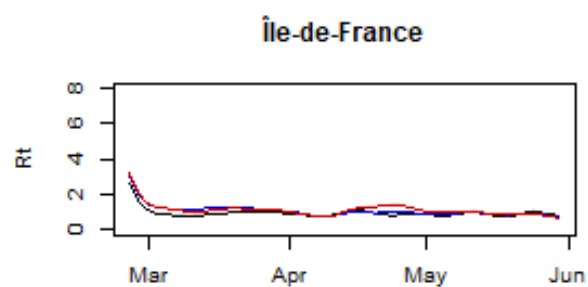
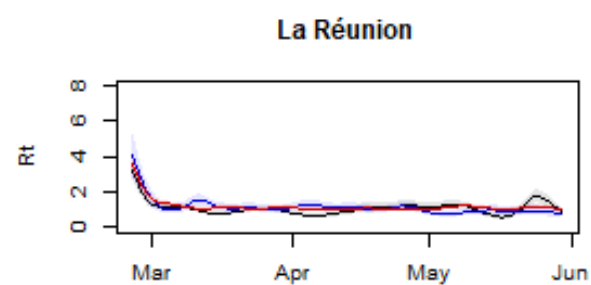
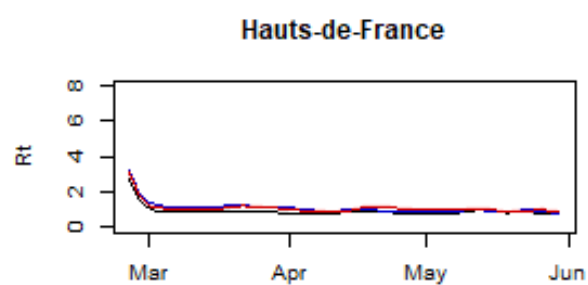
**Pays de la Loire**

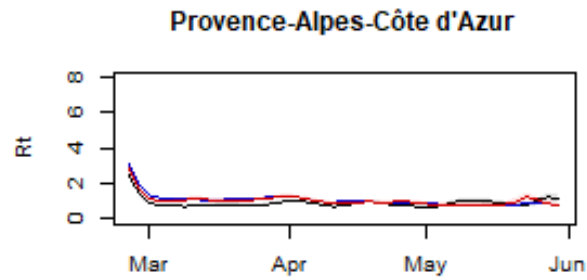
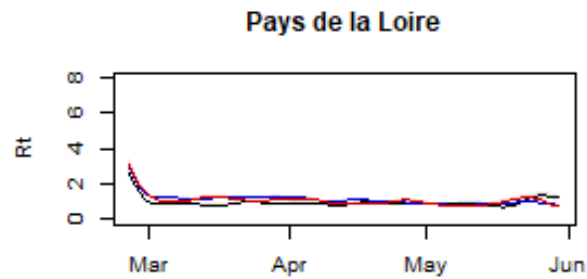


**Provence-Alpes-Côte d'Azur**









## table looking at inclusion

days where 2 variants have Rt estimates with 95%CrI lower than 0.5

```
selection <- select_Rt_get_median_samples(th = 0.2, # only keep where 95%CrI of Rt less then 0.2
                                           EpiEstim_Rt = initial_res$EpiEstim_Rt,
                                           regions = regions,
                                           variants = variants,
                                           SI = SI_assumed,
                                           trim = 0)
```

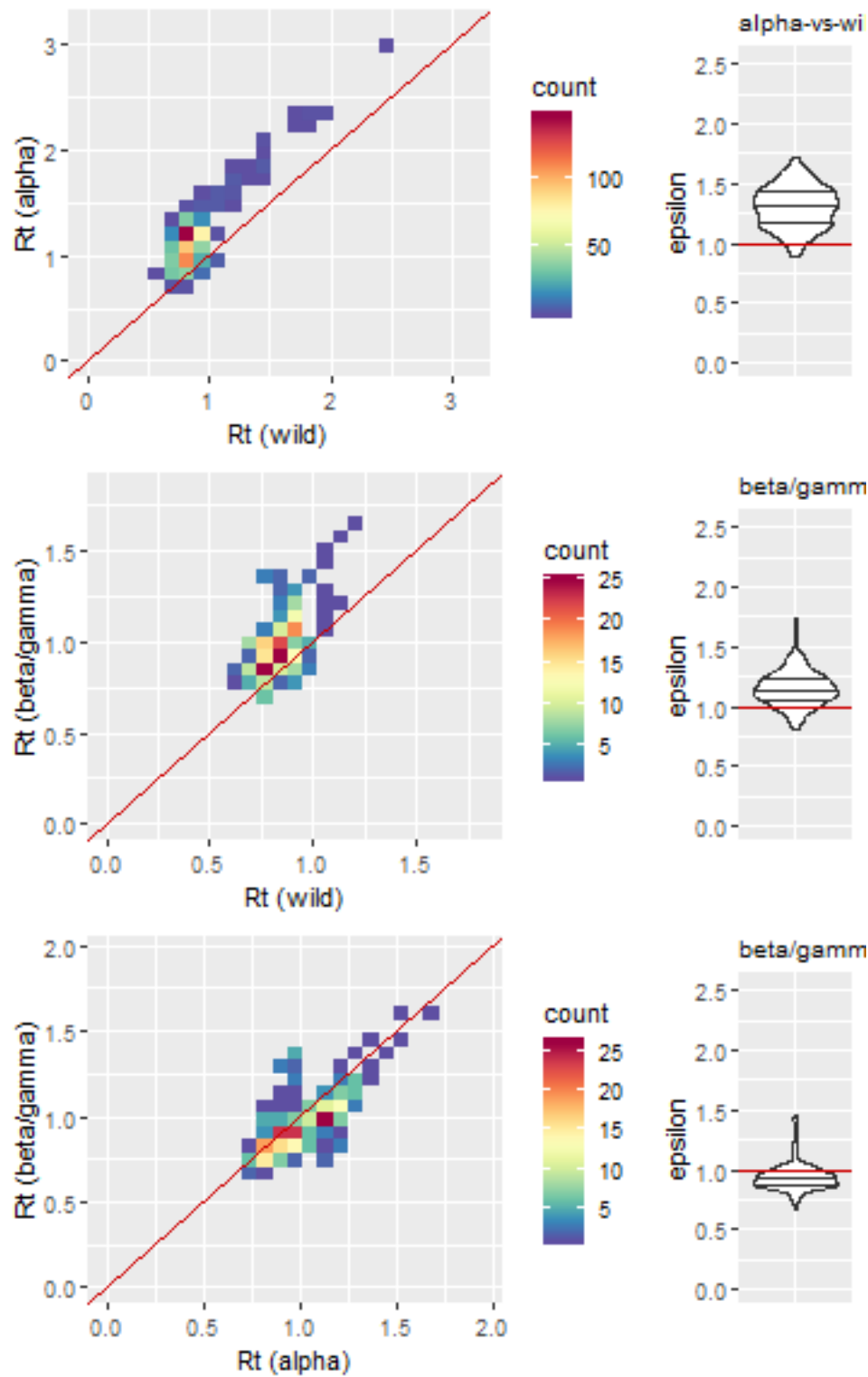
```
selection$summary_select
```

##	region	wild-vs-alpha	wild-vs-beta/gamma
## 1	Auvergne-Rhône-Alpes	73	46
## 2	Bourgogne-Franche-Comté	58	3
## 3	Bretagne	27	0
## 4	Centre-Val de Loire	44	0
## 5	Corse	0	0
## 6	Grand Est	75	74
## 7	Guadeloupe	0	0
## 8	Guyane	0	0
## 9	Hauts-de-France	75	16
## 10	Île-de-France	95	92
## 11	La Réunion	0	0
## 12	Martinique	0	0

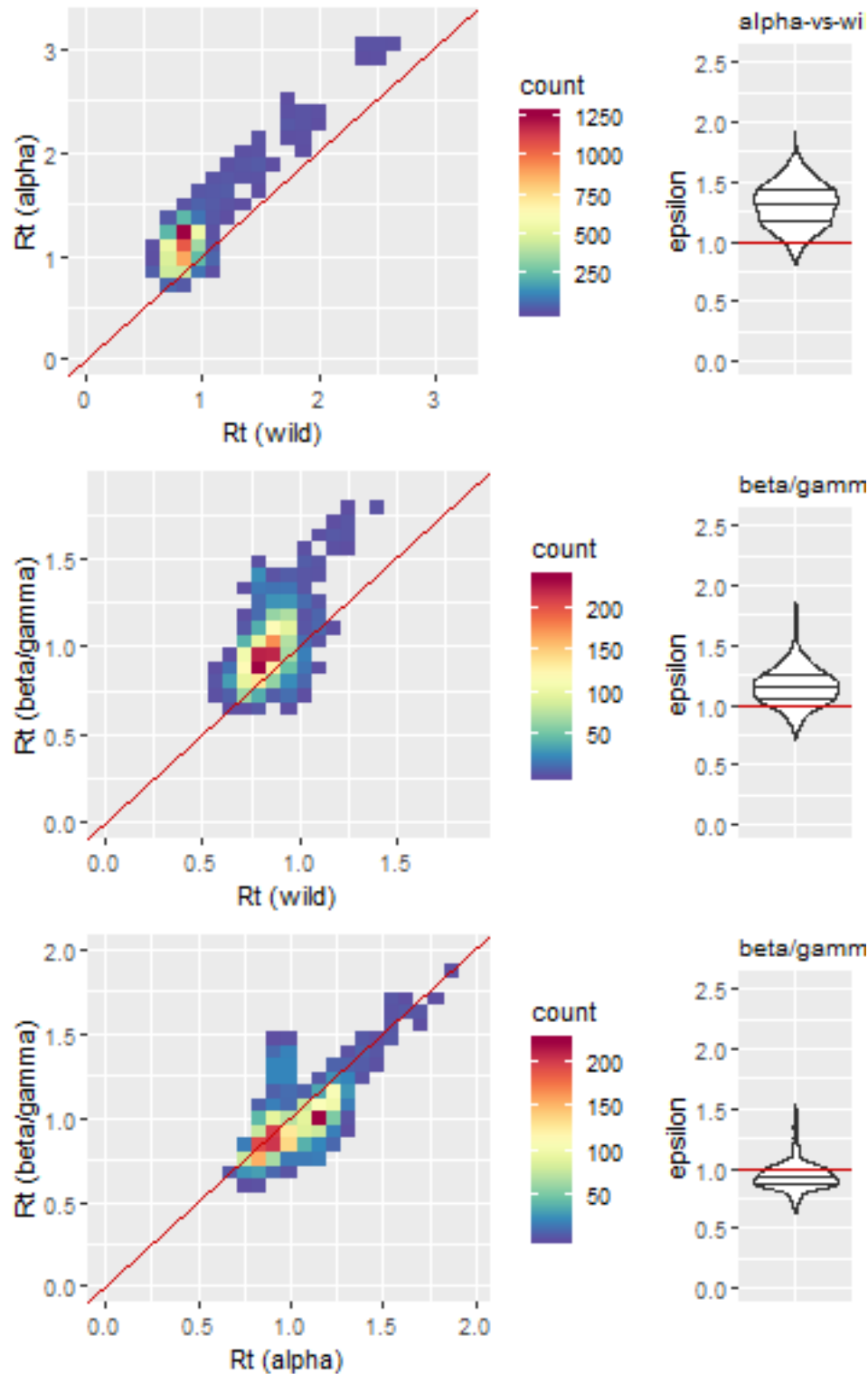
## 13	Mayotte	0	0
## 14	Normandie	56	0
## 15	Nouvelle-Aquitaine	57	0
## 16	Occitanie	70	1
## 17	Pays de la Loire	66	27
## 18	Provence-Alpes-Côte d'Azur	67	22
##	alpha-vs-beta/gamma		
## 1	46		
## 2	3		
## 3	0		
## 4	0		
## 5	0		
## 6	91		
## 7	0		
## 8	0		
## 9	16		
## 10	92		
## 11	0		
## 12	0		
## 13	0		
## 14	0		
## 15	0		
## 16	1		
## 17	32		
## 18	24		

```
plot_hist_dist(x = selection$median_Rts, x_sum = selection$summary_select)
```





```
plot_hist_dist(x = selection$samples_Rts, x_sum = selection$summary_select)
```



```
# second
selection <- select_Rt_get_median_samples(th = 0.2,
  EpiEstim_Rt = initial_res$EpiEstim_Rt,
  regions = regions,
  variants = variants,
```

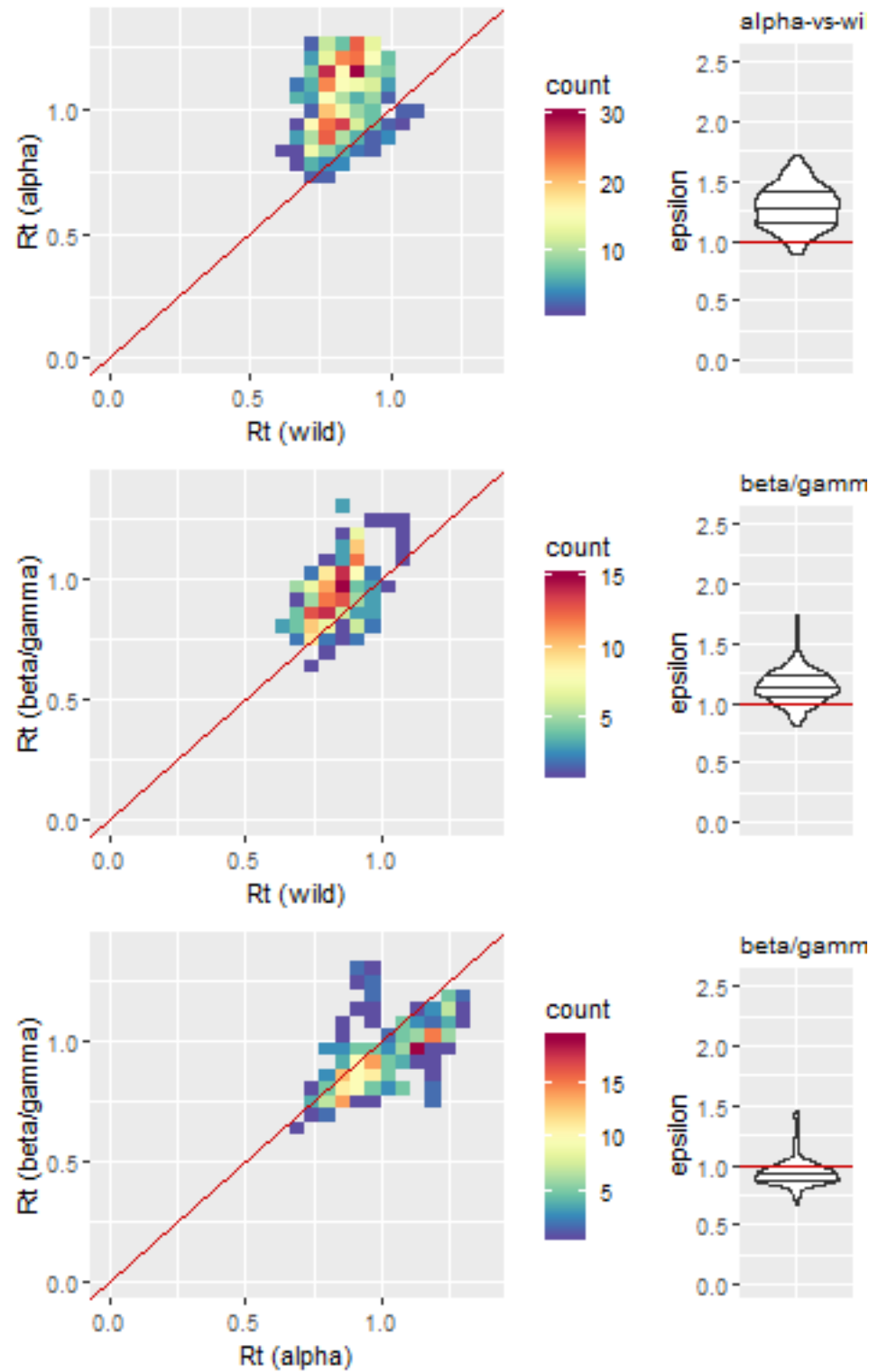
```

SI = SI_assumed,
trim = 0.99) # trim initial Rt until cumsum(1:x)>=0.99
selection$summary_select

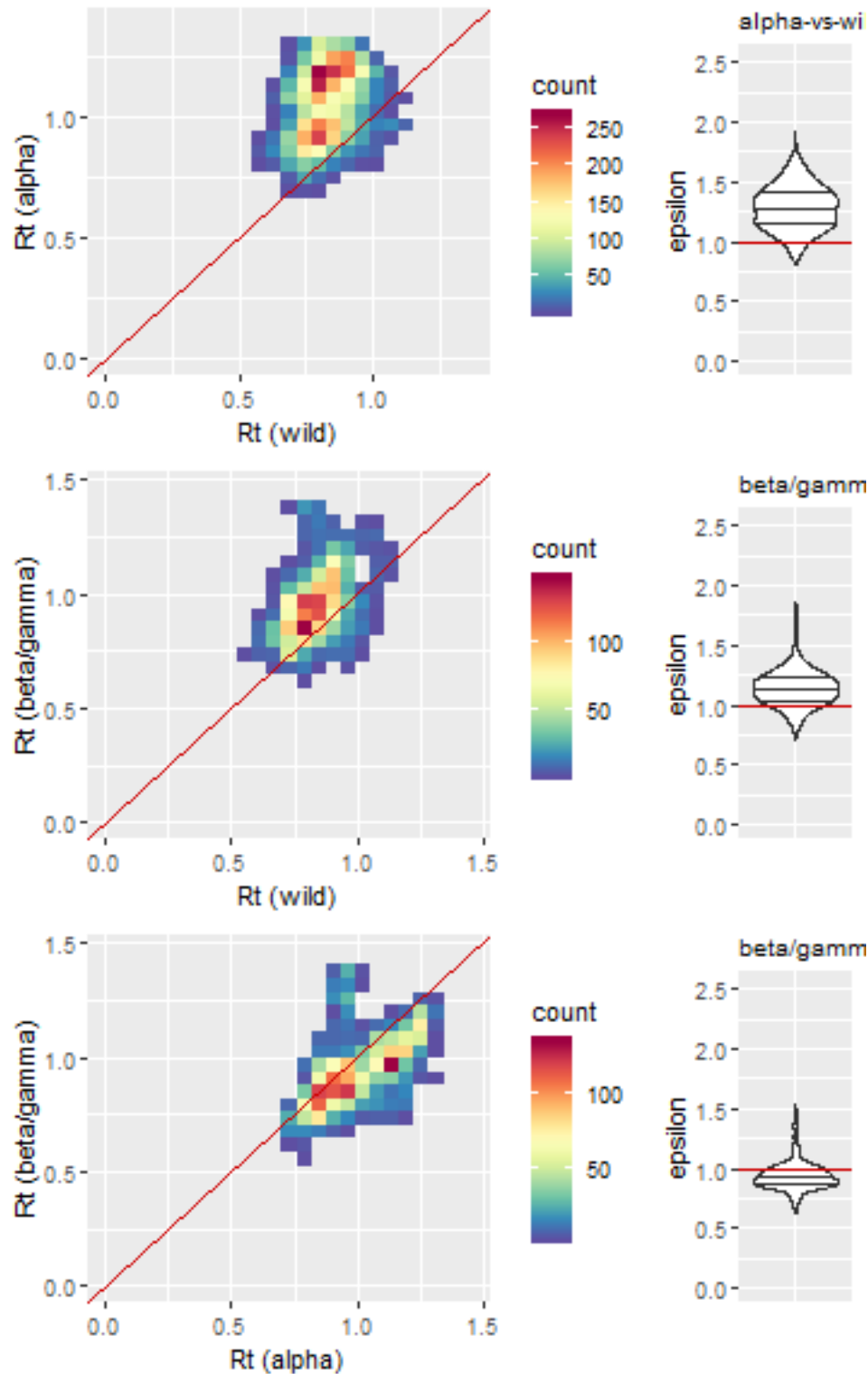
##           region wild-vs-alpha wild-vs-beta/gamma
## 1  Auvergne-Rhône-Alpes          63          46
## 2  Bourgogne-Franche-Comté       51           3
## 3  Bretagne                    19           0
## 4  Centre-Val de Loire          37           0
## 5  Corse                       0           0
## 6  Grand Est                   66          66
## 7  Guadeloupe                   0           0
## 8  Guyane                       0           0
## 9  Hauts-de-France             65          16
## 10 Île-de-France              85          85
## 11 La Réunion                  0           0
## 12 Martinique                  0           0
## 13 Mayotte                     0           0
## 14 Normandie                   48           0
## 15 Nouvelle-Aquitaine          49           0
## 16 Occitanie                   60           1
## 17 Pays de la Loire            57          27
## 18 Provence-Alpes-Côte d'Azur  57          21
##   alpha-vs-beta/gamma
## 1          46
## 2           3
## 3           0
## 4           0
## 5           0
## 6          83
## 7           0
## 8           0
## 9          16
## 10         85
## 11          0
## 12          0
## 13          0
## 14          0
## 15          0
## 16           1
## 17         32
## 18         23

plot_hist_dist(x = selection$median_Rts, x_sum = selection$summary_select)

```



```
ep <- plot_hist_dist(x = selection$samples_Rts, x_sum = selection$summary_select, keep=TRUE)
```



```
res_epsilon <- data.frame(matrix(NA, ncol = 4, nrow = length(u_age) ))
names(res_epsilon) <- c('Age_class', names(ep))
res_epsilon$Age_class <- u_age

for(i in 1:3){
```

```

temp <- round(quantile(ep[[i]],c(0.5,.025,.975)),digits = 2)
res_epsilon[length(u_age),1+i] <- paste0(temp[1], ' ; 95%CrI[' ,temp[2], ' ; ' ,temp[3], ' ]')
}

```

## for 0-9

```

for(j in 1:(length(u_age)-1)){
  print(u_age[j])

  initial_res <- wrapper(age_group = u_age[j], regions = regions, plot_incidence = FALSE,
                        variants = variants, t_window = t_window,
                        SI = SI_assumed, mean_prior = mean_prior,
                        std_prior = std_prior, n_sample_R = n_sample_R, plot_Rt = FALSE)

  selection <- select_Rt_get_median_samples(th = 0.2,
                                           EpiEstim_Rt = initial_res$EpiEstim_Rt,
                                           regions = regions,
                                           variants = variants,
                                           SI = SI_assumed,
                                           trim = 0.99)

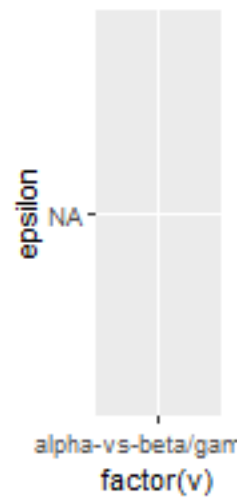
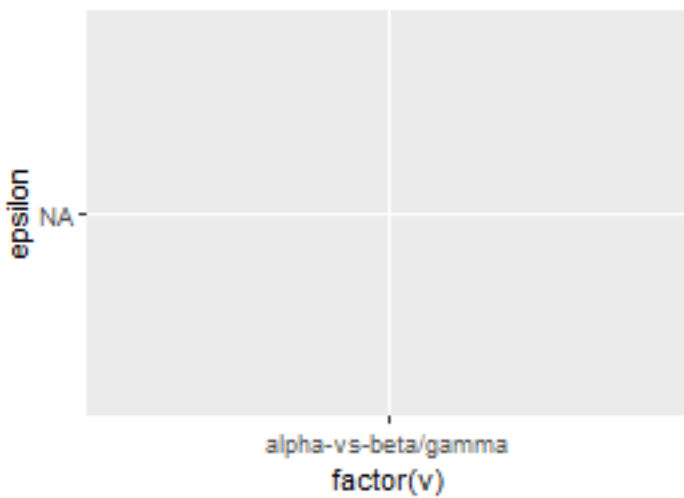
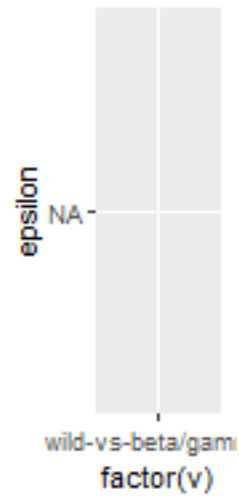
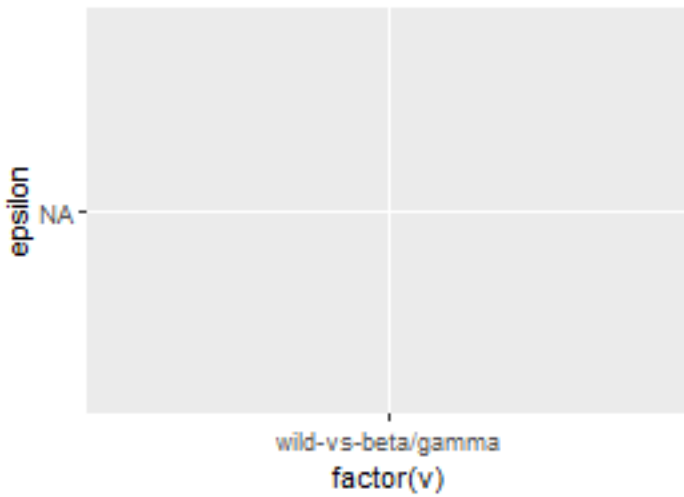
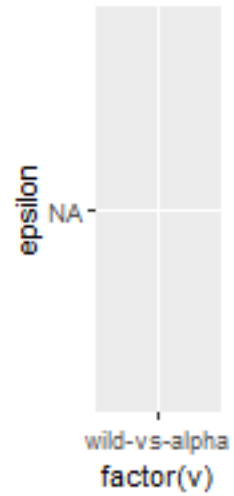
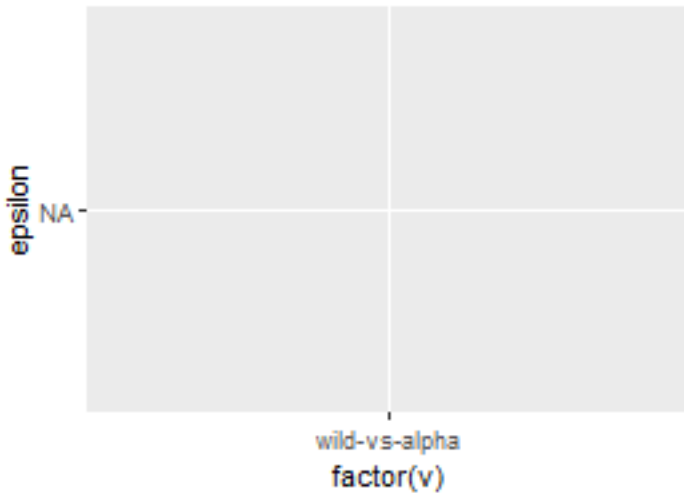
  selection$summary_select

  ep <- plot_hist_dist(x = selection$samples_Rts, x_sum = selection$summary_select, keep=TRUE)

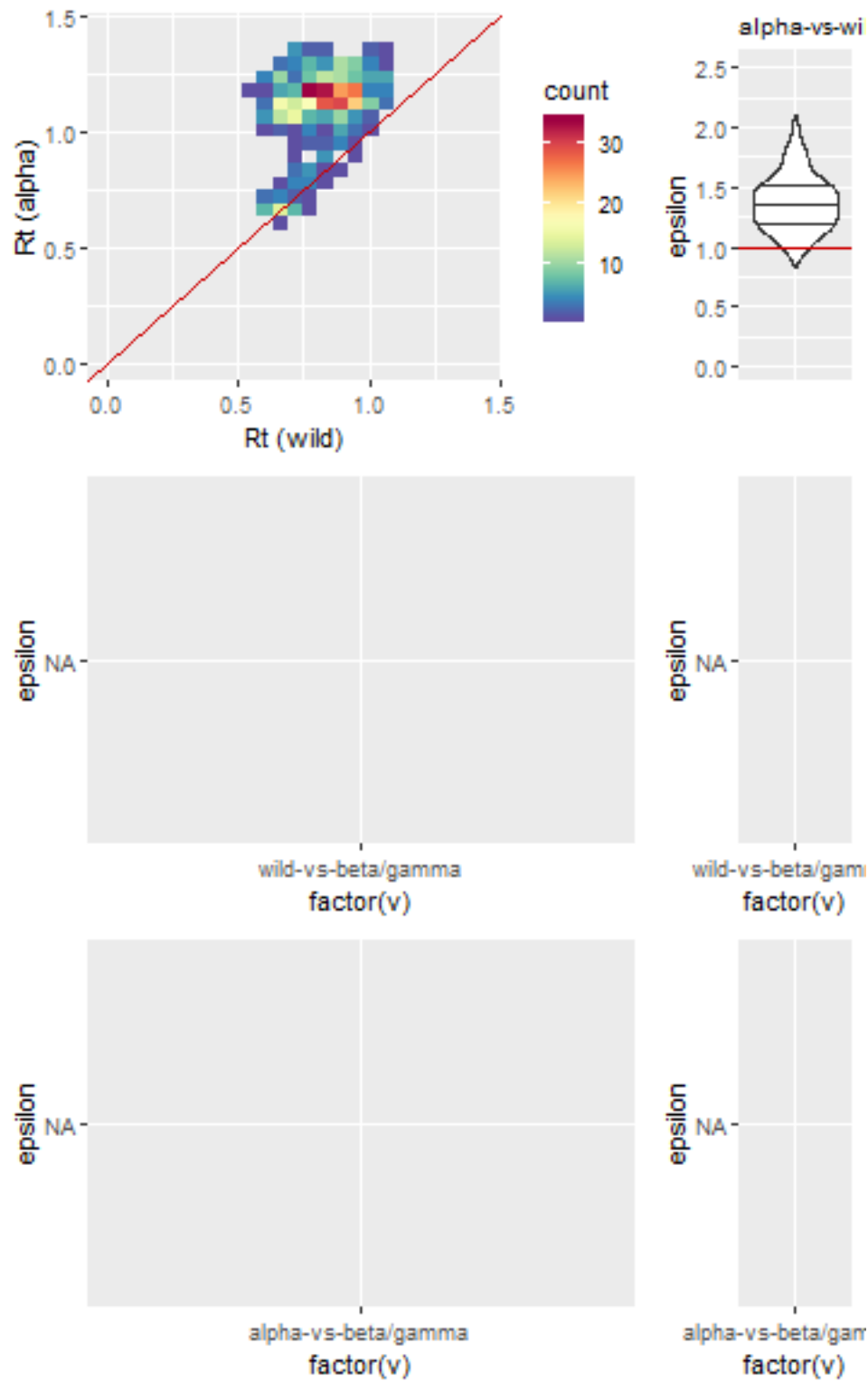
  for(i in 1:3){
    temp <- round(quantile(ep[[i]],c(0.5,.025,.975),na.rm=TRUE),digits = 2)
    res_epsilon[j,1+i] <- paste0(temp[1], ' ; 95%CrI[' ,temp[2], ' ; ' ,temp[3], ' ]')
  }
}

## [1] "9"

```

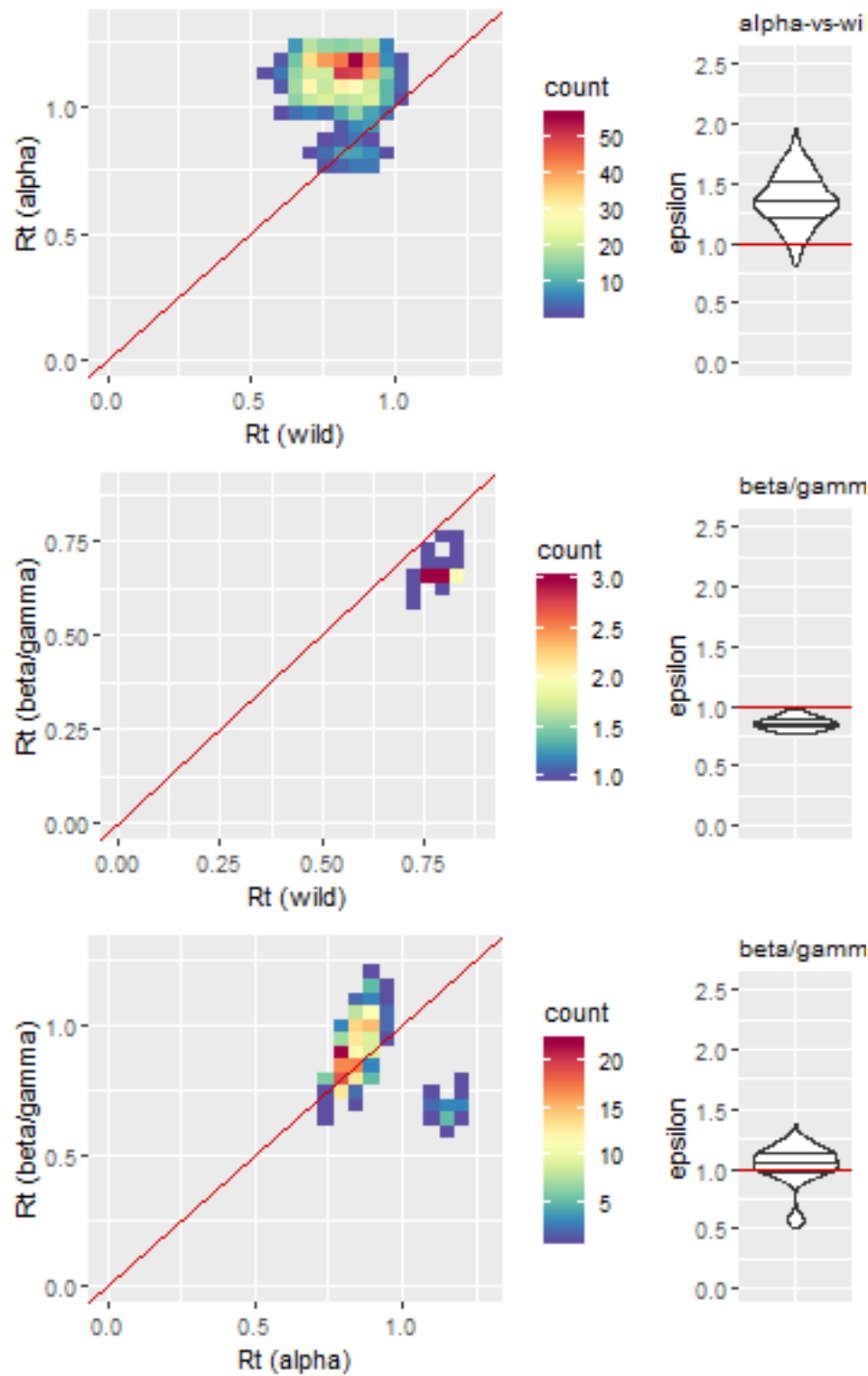


## [1] "19"

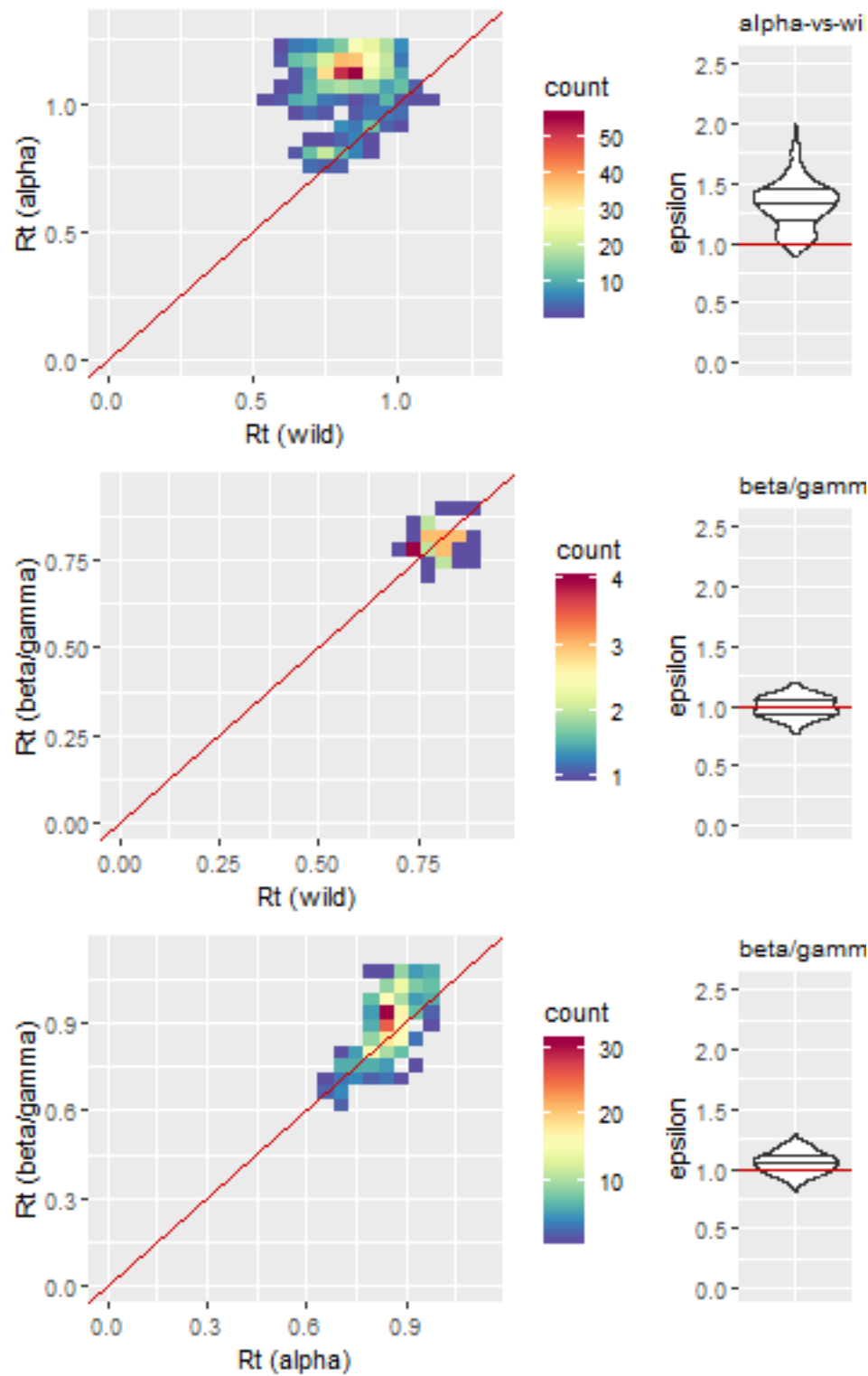


```
## [1] "29"
```

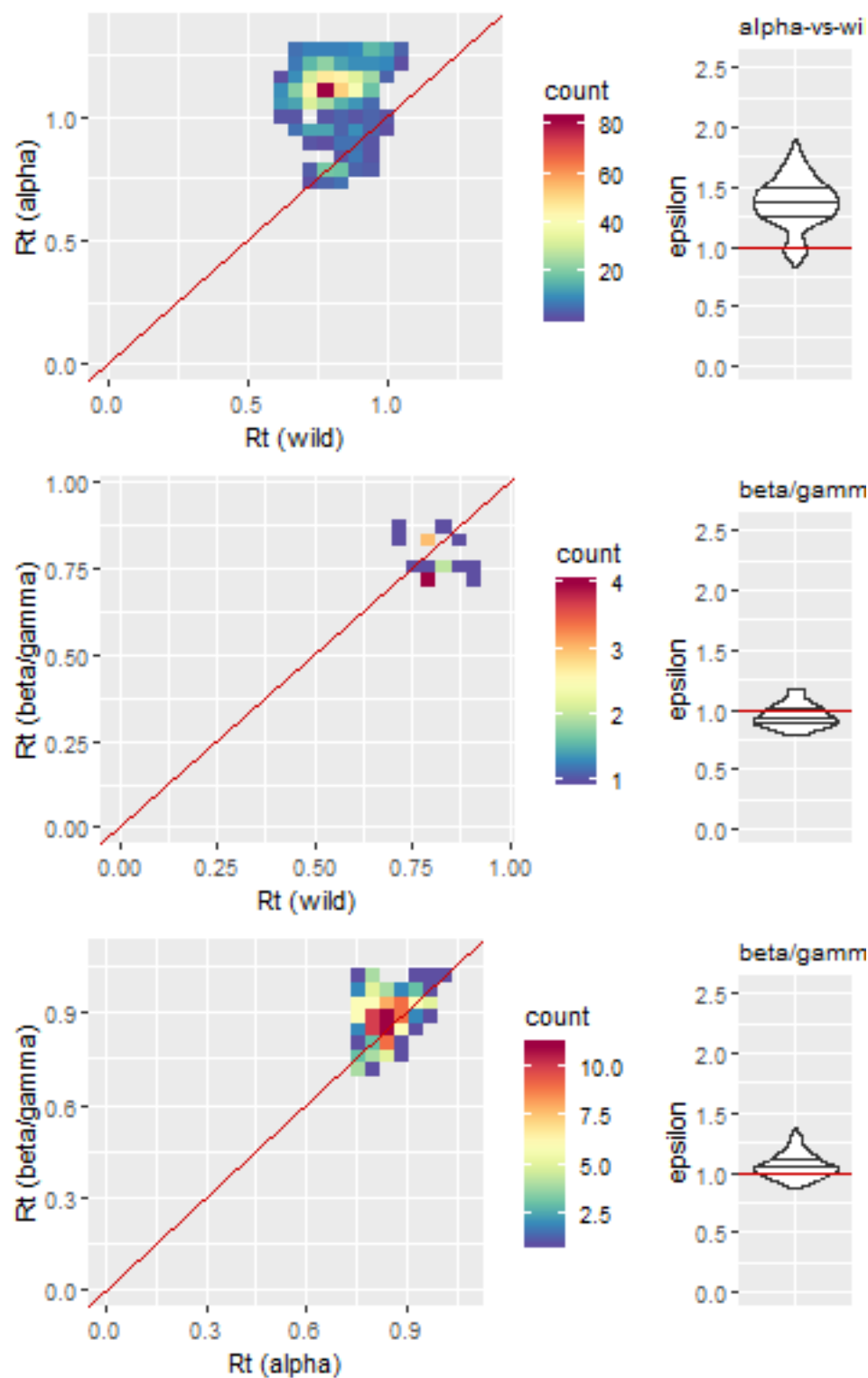




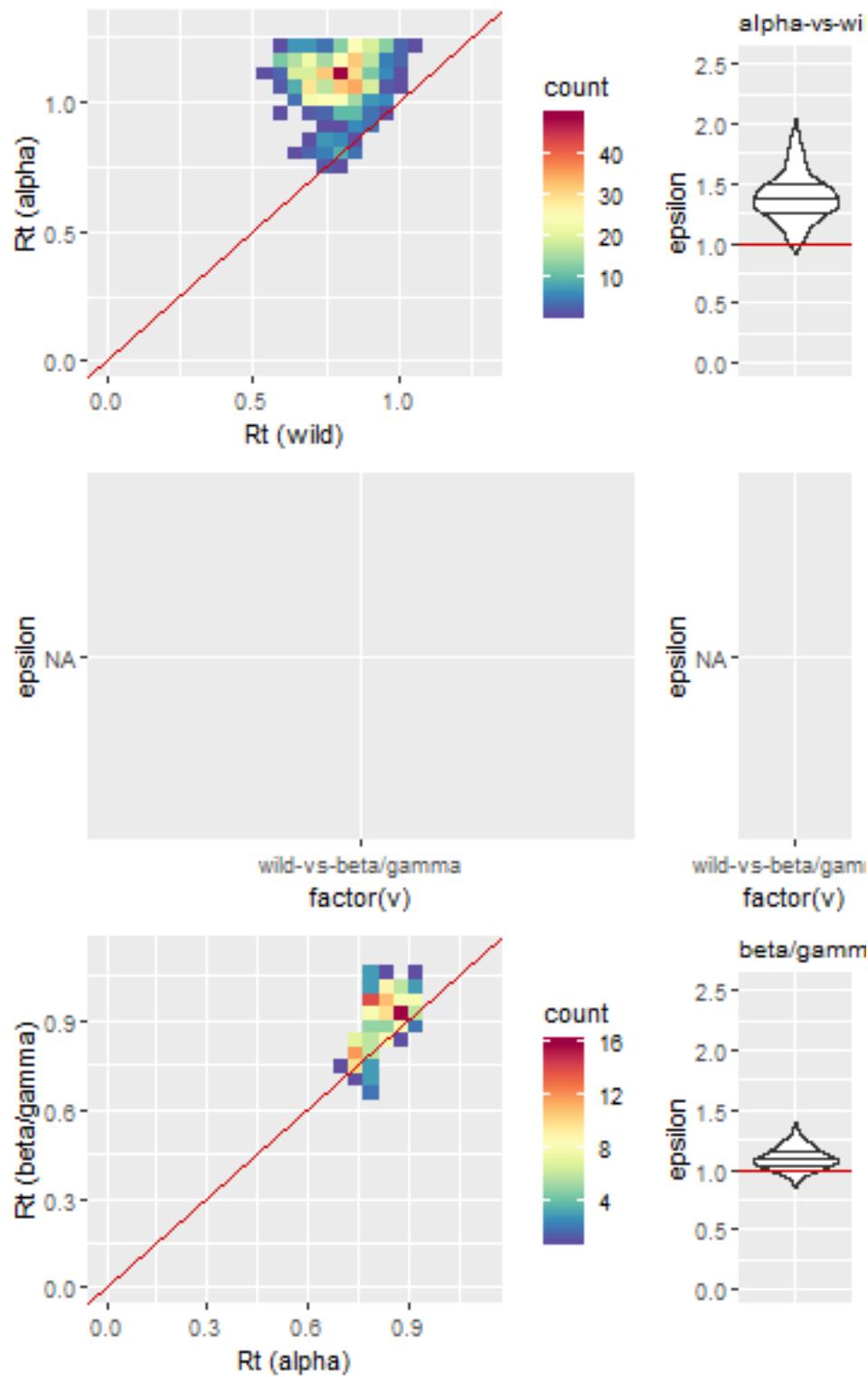
## [1] "39"



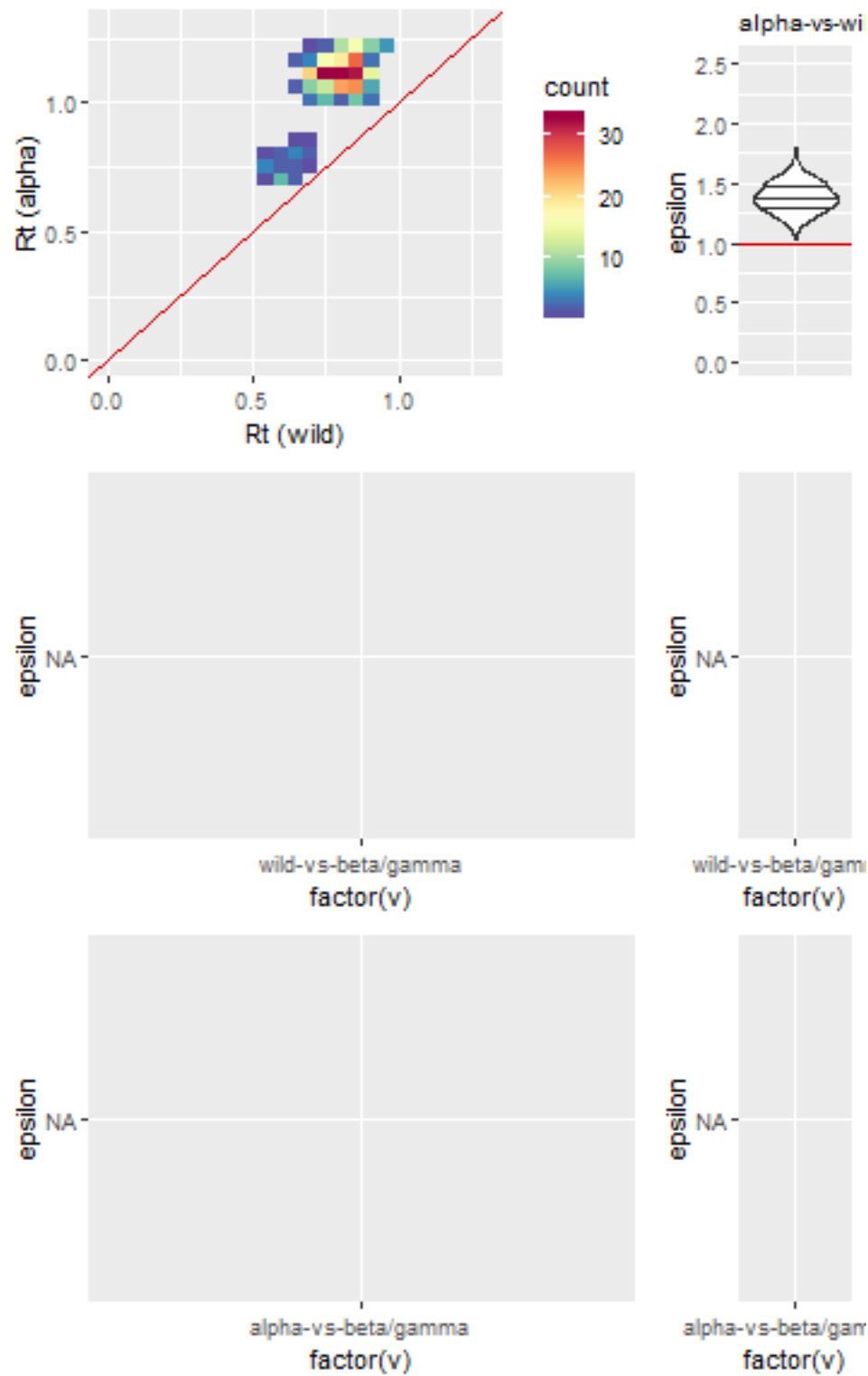
```
## [1] "49"
```



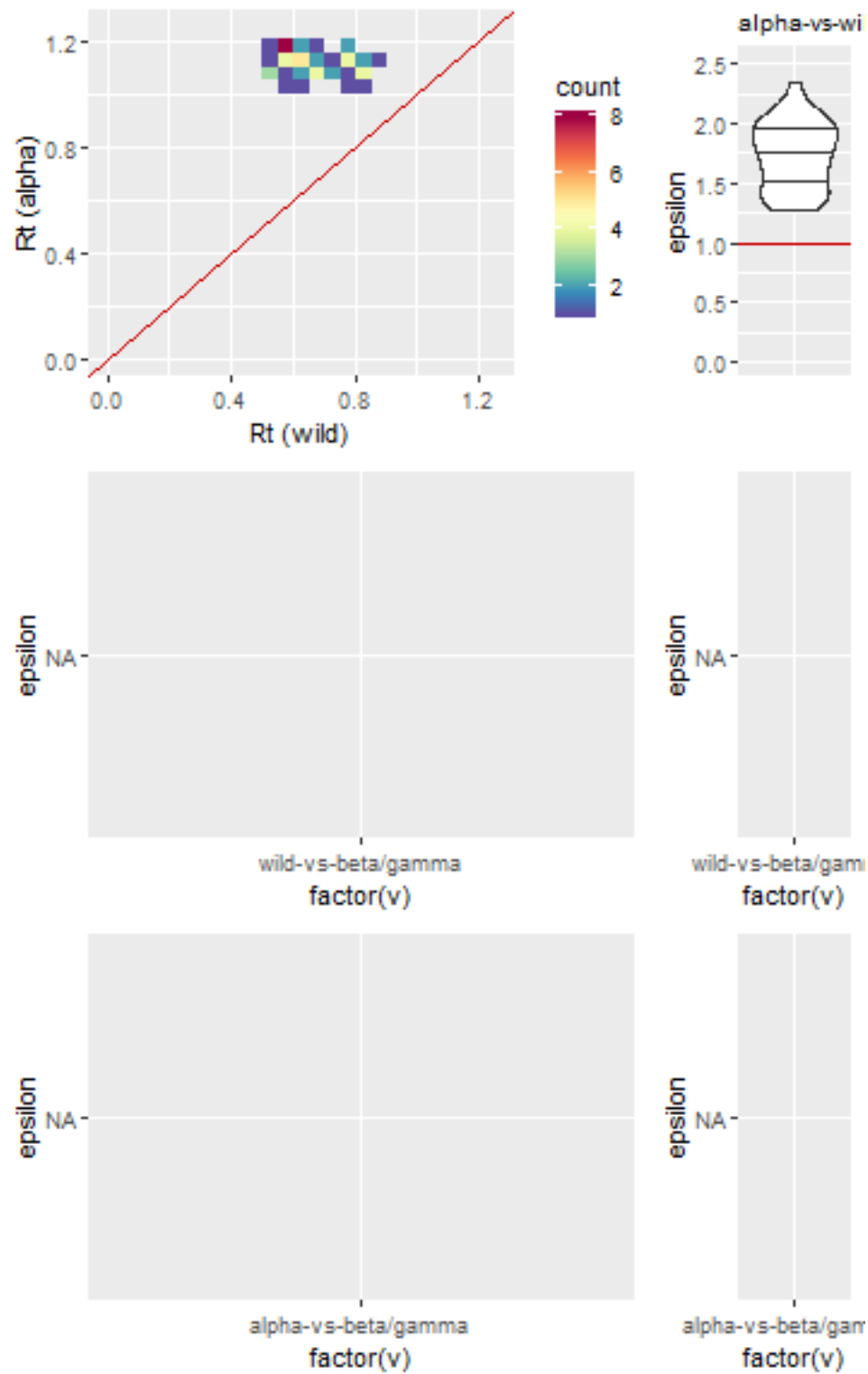
```
## [1] "59"
```



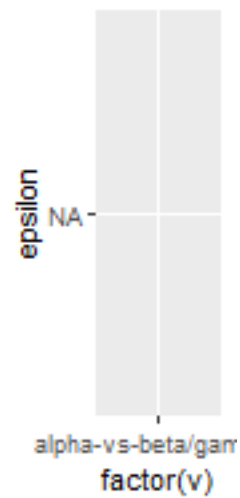
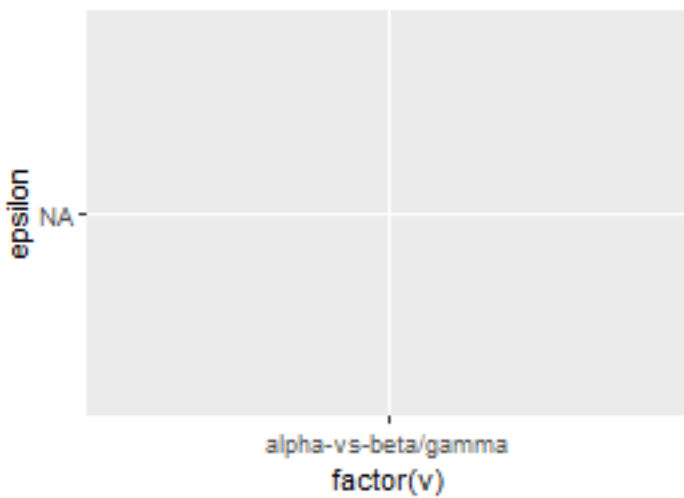
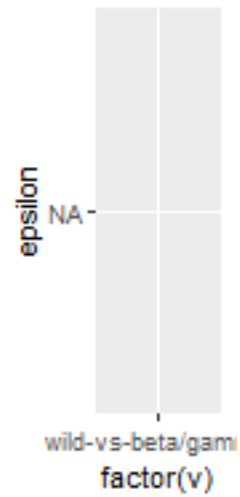
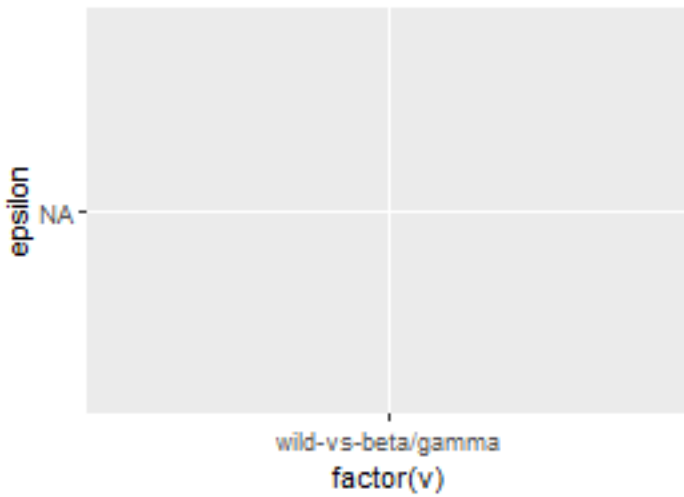
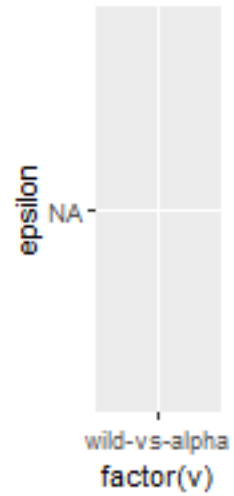
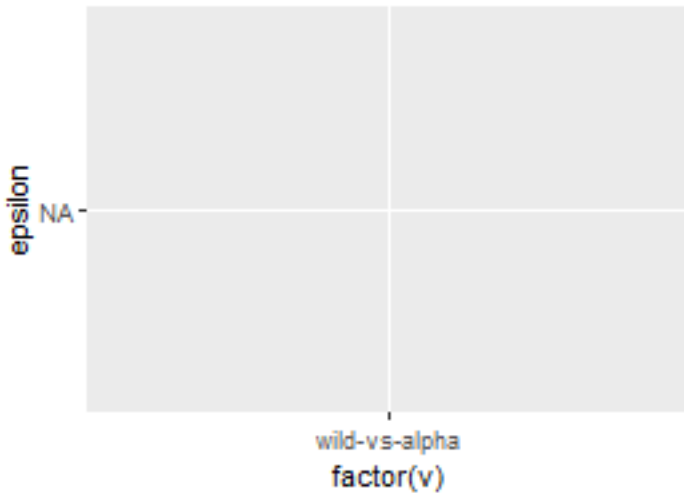
## [1] "69"



## [1] "79"



```
## [1] "89"
```



## [1] "90"

